Fig 1.

```
SEQID22    MLLLGAVLLLLALPGHDQETTTQGPGVLLPLPKGACTGWMAGIPGHPGHNGAPGRDGRDG  60
SEQID23    ------------------------------------------------------------
SEQID24    MLLLGAVLLLLALPGHDQETTTQGPGVLLPLPKGACTGWMAGIPGHPGHNGAPGRDGRDG  60
SEQID25    MLLLGAVLLLLALPGHDQETTTQGPGVLLPLPKGACTGWMAGIPGHPGHNGAPGRDGRDG  60


SEQID22    TPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSVGLE  120
SEQID23    -----------------------MPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSVGLE  36
SEQID24    TPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGA------------  108
SEQID25    TPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGA------------  120


SEQID22    TYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVSLFKKDK  180
SEQID23    TYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVSLFKKDK  96
SEQID24    ------------------------------------------------------------  108
SEQID25    TYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLY----------------------  158


SEQID22    AMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYAD--NDND-STFTGF  237
SEQID23    AMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYAD--NDND-STFTGF  153
SEQID24    ----------------------LLS-PTCPFALPRSSTISKTTMMAP--LVNSTATFLGC  143
SEQID25    ------------------------------------------------------------  158


SEQID22    LLYHDTN---------- 244
SEQID23    LLYHDTN---------- 160
SEQID24    T----T-LP-TTSQSI- 153
SEQID25    ---------LHRLSSLP 166
```

Fig 2.

```
SEQID28   MLLLQALLFLLILPSHAEDDVTTTEELAPALVPPPKGTCAGWMAGIPGHPGHNGTPGRDG  60
SEQID30   MLLLQALLFLLILPSHAEDDVTTTEELAPALVPPPKGTCAGWMAGIPGHPGH--------  52
SEQID29   MLLLQALLFLLILPSHAEDDVTTTEELAPALVPPPKGTCAGWMAGIPGHPGHNGTPGRDG  60
SEQID26   MLLLQALLFLLILPSHAEDDVTTTEELAPALVPPPKGTCAGWMAGIPGHPGHNGTPGRDG  60
SEQID27   ------------------------------------------------------------

SEQID28   ---TPGEKGEKGDAGLLGPKGETGDVGMTGAEGPRGFPGTPGRKGEPGEAA-----AASL  113
SEQID30   ------------------------------------------------------------  52
SEQID29   ---TPGEKGEKGDAGLLGPKGETGDVGMTGAEGPRGFPGTPGRKGEPGEAAY--------  110
SEQID26   RDGTPGEKGEKGDAGLLGPKGETGDVGMTGAEGPRGFPGTPGRKGEPGEAAYMYRSAFSV  120
SEQID27   -------------------------MTGAEGPRGFPGTPGRKGEPGEAAYVYRSAFSV  33

SEQID28   ------------------------------------------------------------  109
SEQID30   ------------------------------------------------------------  52
SEQID29   ------------------------------------------------------------  110
SEQID26   GLETRVTPNVPIRFTKIFYNQQNHYDGSTGKFYCNIPGLYYFSYHITVYMKDVKVSLFK  180
SEQID27   GLETRVTPNVPIRFTKIFYNQQNHYDGSTGKFYCNIPGLYYFSYHITVYMKDVKVSLFK  93

SEQID28   ------------------------------------------------------FPMYP  118
SEQID30   ---------------IKIK-------FEGHP-----PG---------------------  63
SEQID29   ------------------------------------VYRSAFSVGLETRVTVP  129
SEQID26   KDKAVLFTYDQYQEKNVDQA--------SGSVLLHLEVGDQVWLQ--------------  217
SEQID27   KDKAVLFTYDQYQEKNVDQA--------SGSVLLHLEVGDQVWLQ--------------  130

SEQID28   FALLRSSTTNRIIMTAALASSTATFRDSTTSLTTSRCT---  156
SEQID30   --RLNCAKIWHFLQD------------------------  76
SEQID29   NVPIRFTKIFYNQQN-HYDGSTGKFYCNIPGLYIYWLSSLP  169
SEQID26   --VYGDGDHNGLYADNVNDSTFTGFLLYHDTN---------  247
SEQID27   --VYGDGDHNGLYADNVNDSTFTGFLLYHDTN---------  160
```

Fig 3.

```
SEQID31    MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP--------------- 44
SEQID32    MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP------------HVV 47


SEQID31    PAKLQPRALAGWLRPEDGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQD 104
SEQID32    PALPLSNQLCDLEQQRHWASVFSQSTKDSGSDLTVSGRTWGLRV--------------- 91


SEQID31    ILWEEAKEAPADK----------- 117
SEQID32    LNRLFPPSSRERSRRSHQPSCSPEL 116
```

Fig 4.

```
SEQID33    MAFMKKYLLPILGLFMAYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAYHLAKMGAH 60
SEQID38    --------------------------MLQGKKVIVTGASKGIGREMAYHLAKMGAH 30
SEQID36    MAFMKKYLLPILGLFMAYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAYHLAKMGAH 60
SEQID35    MAFMKKYLLPILGLFMAYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAYHLAKMGAH 60
SEQID37    MAFMKKYLLPILGLFMAYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAYHLAKMGAH 60
SEQID39    MAFMKKYLLPILGLFMAYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAYHLAKMGAH 60
SEQID34    MAFMKKYLLPILGLFMAYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAYHLAKMGAH 60


SEQID33    VVVTARSKETLQKVVSHCLELGAASAHYIAGTMEDMTFAEQFVAQAGKLMGGLDMLILNH 120
SEQID38    VVVTARSKETLQKVVSHCLELGAASAHYIAGTMEDMTFAEQFVAQAGKLMGGLDMLILNH 90
SEQID36    VVVTARSKETLQKVVSHCLELGAASAHYIAGTMEDMTFAEQFVAQAGKLMGGLDMLILNH 120
SEQID35    VVVTARSKETLQKVVSHCLELGAASAHYIAGTMEDMTFAEQFVAQAGKLMGGLDMLILNH 120
SEQID37    VVVTASS----------------AHYIAGTMEDMTFAEQFVAQAGKLMGGLDMLILNH 102
SEQID39    VVVTARSKETLQKVVSHCLELGAASAHYIAGTMEDMTFAEQFVAQAGKLMGGLDMLILNH 120
SEQID34    VVVTASS-------:----------AHYIAGTMEDMTFAEQFVAQAGKLMGGLDMLILNH 102


SEQID33    ITNTSLNLFHDDIHHVRKSMEVNFLSYVVLTVAALPMLKQSNGSIVVVSSLAGKVAYPMV 180
SEQID38    ITNTSLNLFHDDIHHVRKSMEVNFLSYVVLTVAALPMLKQSNGSIVVVSSLAGKVAYPMV 150
SEQID36    ITNTSLNLFHDDIHHVR-----------------PMLKQSNGSIVVVSSLAGKVAYPMV 162
SEQID35    ITNTSLNLFHDDIHHVRKSMEVNFLSYVVLTVAALPMLKQSNGSIVVVSSLAGKVAYPMV 180
SEQID37    ITNTSLNLFHDDIHHVRKSMEVNFLSYVVLTVAALPMLKQSNGSIVVVSSLAGKVAYPMV 162
SEQID39    ITNTSLNLFHDDIHHVRKSMEVNFLSYVVLTVAALPMLKQSNGSIVVVSSLA------- 172
SEQID34    ITNTSLNLFHDDIHHVRKSMEVNFLSYVVLTVAALPMLKQSNGSMCAL----------- 150


SEQID33    AAYSASKFALDGFFSSIRKEYSVSRVNVSITLCVLGLIDTETAMKAVSGIVHMQAAPKEE 240
SEQID38    AAYSASKFALDGFFSSIRKEYSVSRVNVSITLCVLGLIDTETAMKAVSGIVHMQAAPKEE 210
SEQID36    AAYSASKFALDGFFSSIRKEYSVSRVNVSITLCVLGLIDTETAMKAVSGIVHMQAAPKEE 222
SEQID35    AAYSASKFALDGFFSSIRKEYSVSRVNVSITLCVLGLIDTETAMKAVSGIVHMQAAPKEE 240
SEQID37    AAYSASKFALDGFFSSIRKEYSVSRVNVSITLCVLGLIDTETAMKAVSGIVHMQAAPKEE 222
SEQID39    ----------------------------------------ETAMKAVSGIVHMQAAPKEE 192
SEQID34    --------------------------------------LLECYHVVHLSSX---- 163


SEQID33    CALEIIKGGALRQEEVYYDSSLWTTLLIRNPCRKILEFLYSTSYNMDRFINK--- 292
SEQID38    CALEIIKGGALRQEEVYYDSSLWTTLLIRNPCRKILEFLYSTSYNMDRFINK--- 262
SEQID36    CALEIIKGGALRQEEVYYDSSLWTTLLIRNPCRKILEFLYSTSYNMDRFINK--- 274
SEQID35    AAYSASKFALDGFFSSIRKEYSVSRVNVSITLCVLGLIDTETAMKAVSGIVHMQAAPKEE 295
SEQID37    CALEIIKGGALRQEEVYYDSSLWTTLLIRNPCRKILEFLYSTSYNMDRFINK--- 274
SEQID39    CALEIIKGGALRQEEVYYDSSLWTTLLIRNPCRKILEFLYSTSYNMDRFINK--- 244
SEQID34    ------------------------------------------------------
```

Fig 5.

```
SEQID40    MAVMKNYLLPILVLFLAYYYYSTNEEFRPEMLQGKKVIVTGASKGIGREMAYHLSKMGAH 60
SEQID41    MAVMKNYLLPILVLFLAY------------------------------------------- 18
SEQID42    MAVMKNYLLPILVLFLAYYYYSTNEEFRPEMLQGKKVIVTGASKGIGREMAYHLSKMGAH 60


SEQID40    VVLTARSEEGLQKVVSRCLELGAASAHYIAGTMEDMTFAEQFIVKAGKLMGGLDMLILNH 120
SEQID41    YYYSTNEEFRLQKVVSRCLELGAASAHYIAGTMEDMTFAEQFIVKAGKLMGGLDMLILNH 78
SEQID42    VVLTARSEEGLQKVVSRCLELGAASAHYIAGTMEDMTFAEQFIVKAGKLMGGLDMLILNH 120


SEQID40    ITQTSLSLFHDDIHSVRRVMEVNFLSYVVMSTAALPMLKQSNGSIAVISSLAGKMTQPMI 180
SEQID41    ITQTSLSLFHDDIHSVRRVMEVNFLSYVVMSTAALPMLKQSNGSIAVISSLAGKMTQPMI 138
SEQID42    ITQTSLSLFHDDIHSVRRVMEVNFLSYVVMSTAALPMLKQSNGSIAVISSLAGGRTVPQQ 180


SEQID40    APYSASKFALDGFFSTIRTELYITKVNVSITLCVLGLIDTETAMKEISGIINAQASPKEE 240
SEQID41    APYSASKFALDGFFSTIRTELYITKVNVSITLCVLGLIDTETAMKEISGIINAQASPKEE 198
SEQID42    RSRSVTPDSRGP------------------------------------------------ 192


SEQID40    CALEIIKGTALRKSEVYYDKSPLTPILLGNPGRKIMEFFSLRYYNKDMFVSN 292
SEQID41    CALEIIKGTALRKSEVYYDKSPLTPILLGNPGRKIMEFFSLRYYNKDMFVSN 250
SEQID42    ---------------------------------------------------
```

Fig 6.

```
SEQID1    CTGATTCCATACCAGAGGGGCTCAGGATGCTGTTGCTGGGAGCTGTTCTACTGCTATTAG
SEQID2    ------------------------------------------------------------
SEQID3    ------------------------------------------------------------
SEQID4    ------------------------------------------------------------


SEQID1    CTCTGCCCGGGCATGACCAGGAAACCACGACTCAAGGGCCCGGAGTCCTGCTTCCCCTGC
SEQID2    ------------------------------------------------------------
SEQID3    ------------------------------------------------------------
SEQID4    ------------------------------------------------------------


SEQID1    CCAAGGGGGCCTGCACAGGTTGGATGGCGGGCATCCCAGGGCATCCGGGCCCATAATGGGG
SEQID2    ------------------------------------------------------------
SEQID3    ------------------------------------------------------------
SEQID4    ------------------------------------------------------------


SEQID1    CCCCAGGCCGTGATGGCAGAGATGGCACCCCTGGTGAGAAGGGTGAGAAAGGAGATCCAG
SEQID2    ---------------------ATG------------------------------------
SEQID3    ---------------------CTGATTCCAT-----------------------------
SEQID4    ---------------------CTGATTCCAT-----------------------------
                               **


SEQID1    GTCTTATTGGTCCTAAGGGAGACATCGGTGAAACCGGAGTACCCG--GGGCTGAAGGTCC
SEQID2    -----------------------------------------ACCCG--GGGCTGAAGGTCC
SEQID3    ------------------------------------------ACCAGAGGGGCTCAGGATGC
SEQID4    ------------------------------------------ACCAGAGGGGCTCAGGATGC
                                                    *** * ***** * * * *


SEQID1    -----CCGAG-GCT-TTC--CGGG-AAT-------CCAAGGCAGGAA-AGGAGAACCTGG
SEQID2    -----CCGAG-GCT-TTC--CGGG-AAT-------CCAAGGCAGGAA-AGGAGAACCTGG
SEQID3    TGTTGCTGGGAGCTGTTCTACTGCTATTAGCTCTGCCCGGGCATGACCAGGA-AACCACG
SEQID4    TGTTGCTGGGAGCTGTTCTACTGCTATTAGCTCTGCCCGGGCATGACCAGGA-AACCACG
              * * *** ***   * *   * *      **  **** ** **** ****   *


SEQID1    A--GAAGGTGCCTATGTA----TACCGCT---CA-----GCATTCAGTG-TGGGATTGGA
SEQID2    A--GAAGGTGCCTATGTA----TACCGCT---CA-----GCATTCAGTG-TGGGATTGGA
SEQID3    ACTCAAGGGCCCGGAGTCCTGCTTCCCCTGCCCAAGGGGGCCGTGATGGCAGAGATGGCGG
SEQID4    ACTCAAGGGCCCGGAGTCCTGCTTCCCCTGCCCAAGGGGGCTGCACAGGTTGGATGGCGG
              *  **** **  **     **** *    **   **    * *  *  *  ****


SEQID1    GACTTACGTTACTATCC---CCAACATG----CCCATTCGCT--TTACCAAGAT------
SEQID2    GACTTACGTTACTATCC---CCAACATG----CCCATTCGCT--TTACCAAGAT------
SEQID3    GGCATCCCAGGGCATCCGGGCCCATAATGGGGCCCCAGGCCGTGATGGCAGAGATGGCACC
SEQID4    GGCATCCCAGGGCATCCGGGCCCATAATGGGGCCCCAGGCCGTGATGGCAGAGATGGCACC
            * * *    **** *** ***  **** * *  *   * ****


SEQID1    -CTTCT-ACAA---TCAGCAA----AACCAC-TATGATGGCTCCACTGGTAAATTCCACT
SEQID2    -CTTCT-ACAA---TCAGCAA----AACCAC-TATGATGGCTCCACTGGTAAATTCCACT
SEQID3    CCTGGTGAGAAGGGTGAGAAAGGAGATCCAGGTCTTATTGGTCCTAAGGGAGACATCGGT
SEQID4    CCTGGTGAGAAGGGTGAGAAAGGAGATCCAGGTCTTATTGGTCCTAAGGGAGACATCGGT
             **   * **   * ** **    * *** * ** * **  *** ** *    * *


SEQID1    GCAAC---ATT--CCTGGGCTGTA---CTACTTTGCCTACCACATCACAGTCTATATGAA
SEQID2    GCAAC---ATT--CCTGGCTGTA---CTACTTTGCCTACCACATCACAGTCTATATGAA
SEQID3    GAAACCGGAGTACCCGGGGCTGAAGGTCCCCGAGGCTTTCCGGG----AATCCA-AGGCA
SEQID4    GAAACCGGAGTACCCGGGGCTGAAGGTCCCCGAGGCTTTCCGGG----AATCCA-AGGCA
            * ***  * *  ** ****** *   *  ** *   ** * **    * ** *** *


SEQID1    GGATGTGAAGGTCAGCCTCTTCAAGAAGGACAAGGCTATGC---TCTTCACCTATGATCA
SEQID2    GGATGTGAAGGTCAGCCTCTTCAAGAAGGACAAGGCTATGC---TCTTCACCTATGATCA
SEQID3    GGA----AAGGAGAACCT--------GGAGAAGG---TGC--------------------
SEQID4    GGA----AAGGAGAACCT--------GGAGAAGG--TGCCTATGTATACCGCTCAGCA
            ***    **** * ***       *** **** * ***


SEQID1    GTACCAGGAAAATAATGTGGACC---AGGCCTCCGGCTCTGTGTCCTGCATCTGGAGGT
```

```
SEQID2    GTACCAGGAAAATAATGTGGACC---AGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGT
SEQID3    -----------------------------------GTTACTATCC-CCAACATGCCCATTC
SEQID4    TT--CAG--------TGTGGGATTGGAGACTTACGTTACTATCC-CCAACATGCCCATTC
                             *   ** * * **   ***     *


SEQID1    GGGCGACCAAG-TCTGGCTCCAGGTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTG
SEQID2    GGGCGACCAAG-TCTGGCTCCAGGTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTG
SEQID3    GCTTTACCAAGATCTT-CTACA-----ATCAGCAAAACCACTATGATGG-CTCCA--CTG
SEQID4    GCTTTACCAAGATCTT-CTACA-----ATCAGCAAAACCACTATGATGG-CTCCA--CTG
          *   ****** ***   ** **       ** *  **    *   *  **** *** *   ***


SEQID1    ATAA-TGACAATG----ACTCC--------AC----------------------------
SEQID2    ATAA-TGACAATG----ACTCC--------AC----------------------------
SEQID3    GTAAATTCCACTGCAACATTCCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATA
SEQID4    GTAAATTCCACTGCAACATTCCTGGGCTGTAC----------------------------
          *** *  ** **    * ***        **


SEQID1    ------------------------------------------------------------
SEQID2    ------------------------------------------------------------
SEQID3    TGAAGGATGTGAAGGTCAGCCTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATC
SEQID4    ------------------------------------------------------------


SEQID1    ------------------------------------------------------------
SEQID2    ------------------------------------------------------------
SEQID3    AGTACCAGGAAAATAATGTGGACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGG
SEQID4    ------------------------------------------------------------


SEQID1    ------------------------------------------------------------
SEQID2    ------------------------------------------------------------
SEQID3    GCGACCAAGTCTGGCTCCAGGTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATA
SEQID4    ------------------------------------------------------------


SEQID1    ---------------CTTCACAGGCTTTCTTCTCTACCATGACACCAACTGATCACCAC
SEQID2    ---------------CTTCACAGGCTTTCTTCTCTACCATGACACCAACTGA-------
SEQID3    ATGACAATGACTCCACCTTCACAGGCTTTCTTCTCTACCATGACACCAACTGA-------
SEQID4    ---------------CTTCACAGGCTTTCTTCTCTACCATGACACCAACTGA-------
                         *****************************************


SEQID1    TAACTCAGAGCCTCCTCCAGGCCAAACAGCCCCAAAGTCAATTAAAGGCTTTCAGTACGG
SEQID2    ------------------------------------------------------------
SEQID3    ------------------------------------------------------------
SEQID4    ------------------------------------------------------------


SEQID1    TTAGGAAGTTGATTATTATTTAGTTGGAGGCCTTTAGATATTATTCATTCATTTACTCAT
SEQID2    ------------------------------------------------------------
SEQID3    ------------------------------------------------------------
SEQID4    ------------------------------------------------------------
```

Fig 7.

```
SEQID5   ATGAGACCTGGCCACTTTCTCCTCATTTCTGTCTGTACGATTGTCAGTGGATCTGACGAC  60
SEQID6   ------------------------------------GCTCATTCATCTTTTAATTCA-----  21
SEQID7   ATGAGACCTGGCCACTTTCTCCTCATTTCTGTCTGTACGATTGTCAGTGGATCTGACGAC  60
SEQID8   ------------------------------------------------------------
SEQID9   ------------------------------------------------------------


SEQID5   ACCAAAAGGGCTCAGGATGCTACTGTTGCAAGCTCTCCTGTTCCTCTTAATCCTGCCCAG  120
SEQID6   CCCATAAAGGCTTTGAAAACTAAGGCTGGAGATGAACTTAT-----AGGAGCCTGCCAGG  76
SEQID7   ACCAAAAGGGCTCAGGATGCTACTGTTGCAAGCTCTCCTGTTCCTCTTAATCCTGCCCAG  120
SEQID8   ------------------------------------------------------------
SEQID9   ------------------------------------------------------------


SEQID5   TCATGCCGAAGATGACGTTACTACAACTGAAGAGCTAGCTCCTGCTTTGGTCCCTCCACC  180
SEQID6   CCGTG--GAGAGTGAGGAAGCAGAGATGACGGAGATGATGTCTTTCCTTGTCCTGTGA--  132
SEQID7   TCATGCCGAAGATGACGTTACTACAACTGAAGAGCTAGCTCCTGCTTTGGTCCCTCCACC  180
SEQID8   ------------------------------------------------------------
SEQID9   ------------------------------------------------------------


SEQID5   CAAGGGAACTTGTGCAGGTTGGATGGCAGGCATCCCAGGACATCCTGGCCACAATGGCAC  240
SEQID6   -AATGGATTGTGGGGTAGA---GGTTCCGGAGATAATGCCTCTTGCTGGAAACAGT-----  183
SEQID7   CAAGGGAACTTGTGCAGGTTGGATGGCAGGCATCCCAGGACATCCTGGCCACAATGGCAC  240
SEQID8   ------------------------------------------------------------
SEQID9   ------------------------------------------------------------


SEQID5   ACCAGGCCGTGATGGCAGAGATGGCACTCCTGGAGAGAAGGGAGAGAAAGGAGATGCAGG  300
SEQID6   -CTGGGCAGTTCTGTT---CCCGCCATTC----ACAGAATTCTTCTCACTT---TCTAGG  232
SEQID7   ACCAGGCCGTGATGGCAGAGATGGCACTCCTGGAGAGAAGGGAGAGAAAGGAGATGCAGG  300
SEQID8   ------------------------------------------------------------
SEQID9   ------------------------------------------------------------


SEQID5   TCTTCTTGGTCCTAAGGGTGAGACAGGAGATGTTGGAATGACAGGAGCTGAAGGGCCACG  360
SEQID6   TCTTCTTGGTCCTAAGGGTGAGACAGGAGATGTTGGAATGACAGGAGCTGAAGGGCCACG  292
SEQID7   TCTTCTTGGTCCTAAGGGTGAGACAGGAGATGTTGGAATGACAGGAGCTGAAGGGCCACG  360
SEQID8   ------------------------------------------------------------
SEQID9   ------------------------------------------------------------


SEQID5   GGGCTTCCCGGAACCCCTGGCAGGAAAGGAGAGCCTGGAGAAGCCGCTTATGTGTATCG  420
SEQID6   GGGCTTCCCGGAACCCCTGGCAGGAAAGGAGAGCCTGGAGAAGCCGCTTATGTGTATCG  352
SEQID7   GGGCTTCCCGGAACCCCTGGCAGGAAAGGAGAGCCTGGAGAAGCCGC------------  408
SEQID8   ------------------------------------------------------------
SEQID9   ------------------------------------------------------------


SEQID5   CTCAGCGTTCAGTGTGGGGCTGGAGACCCGCGTCACTGTTCCCAATGTACCCATTCGCTT  480
SEQID6   CTCAGCGTTCAGTGTGGGGCTGGAGACCCGCGTCACTGTTCCCAATGTACCCATTCGCTT  412
SEQID7   --------------------------GTCACTGTTCCCAATGTACCCATTCGCTT  437
SEQID8   --------------------------------ATGAGACC--TGGCCACTTTCTCCT  23
SEQID9   --------------------------------ATGAGACC--TGGCCACTTTCTCCT  23
                                          **    **  **  * * *** * *

SEQID5   TACTAAGATCTTCTACAACCAACAGAATCATTATGACGGCAGCACTGGCAAGTTCTACTG  540
SEQID6   TACTAAGATCTTCTACAACCAACAGAATCATTATGACGGCAGCACTGGCAAGTTCTACTG  472
SEQID7   TACTAAGATCTTCTACAACCAACAGAATCATTATGACGGCAGCACTGGCAAGTTCTACTG  497
SEQID8   CATTTCTGTCTG-TACGATTGTCAG--TGGATCTGACGACACCAAAAG-GGCTCAGGATG  79
SEQID9   CATTTCTGTCTG-TACGATTGTCAG--TGGATCTGACGACACCAAAAG-GGCTCAGGATG  79
         * *   ***  *** *  ***   *  * ***** ** **    *   *    **

SEQID5   CAACATTCCGGGACTCTACTACTTCTCTTACCACATCACGGTGTACATGAAAGATGTGAA  600
SEQID6   CAACATTCCGGGACTCTACTACTTCTCTTACCACATCACGGTGTACATGAAAGATGTGAA  532
SEQID7   CAACATTCCGGGACTCTACTACTTCTCTTACCACATCACGGTGTACATGAAAGATGTGAA  557
SEQID8   CTACTGTTGCAAGCTCTCCTGTTCCTCTTAATCCTGCCCAGT---CATGCCGAAGATGAC  136
SEQID9   CTACTGTTGCAAGCTCTCCTGTTCCTCTTAATCCTGCCCAGT---CATGCCGAAGATGAC  136
```

```
                 *  **  *      ****  **  * ******  *  *  *  **    ****    *  ***

SEQID5    GGTGAGCCTCTTCAAGAAGGACAAGGCCGTTCTCTTCACCTACGACCAGTATCAGGAAAA 660
SEQID6    GGTGAGCCTCTTCAAGAAGGACAAGGCCGTTCTCTTCACCTACGACCAGTATCAGGAAAA 592
SEQID7    GGTGAGCCTCTTCAAGAAGGACAAGGCCGTTCTCTTCACCTACGACCAGTATCAGGAAAA 617
SEQID8    GTTACTACAACT---GAAGAGCTAGCTCCTGCTTTGGTCCCTCCACCCA----AGGGAAC 189
SEQID9    GTTACTACAACT---GAAGAGCTAGCTCCTGCTTTGGTCCCTCCACCCA----AGGGAAC 189
          * *    *   *    ****  *  **  * * ** *   **  * ***     ***  **

SEQID5    GAATGTGGACCAGGCCTCTGGCTCTGTGCTCCTCCATCTGGAGGTGGGAGACCAAGTCTG 720
SEQID6    GAATGTGGACCAGGCCTCTGGCTCTGTGCTCCTCCATCTGGAGGTGGGAGACCAAGTCTG 652
SEQID7    GAATGTGGACCAGGCCTCTGGCTCTGTGCTCCTCCATCTGGAGGTGGGAGACCAAGTCTG 677
SEQID8    TTGTGCAGGTTGGATGGCAGGCATCCCAGGACATC--CTGGCCACAATG----GCACACC 243
SEQID9    TTGTGCAGGTTGGATGGCAGGCATCCCAGGACATC--CTGGCCACATAA----AAATATA 243
          **  *  *   *  ***  *   *   * *  ****

SEQID5    GCTCCAGGTGTATGGGGATGGGGACCACAATGGACTCTATGCAGATAACGTCAACGACTC 780
SEQID6    GCTCCAGGTGTATGGGGATGGGGACCACAATGGACTCTATGCAGATAACGTCAACGACTC 712
SEQID7    GCTCCAGGTGTATGGGGATGGGGACCACAATGGACTCTATGCAGATAACGTCAACGACTC 737
SEQID8    AGGCCGTGATGGCAGAGA-TGGCACTCCTGGA----GAGAAGGGAGAGAAAGGA-GATGC 297
SEQID9    ATTC----------GAGG-GGCATCCACCAGG----CCGGCTGAATTGTGCCAA-AATAT 287
          *        *  *  * *   *  *  *

SEQID5    TACATTTACTGGCTTTCTTCTCTACCATGATACCAACTGACTGCAACTACCCATAGCCCA 840
SEQID6    TACATTTACTGGCTTTCTTCTCTACCATGATACCAACTGACTGCAACTACCCATAGCCCA 772
SEQID7    TACATTTACTGGCTTTCTTCTCTACCATGATACCAACTGACTGCAACTACCCATAGCCCA 797
SEQID8    AGGTCTTCTTGGTCCTAAGGGTGAGACAGGAGATGTTGGAATGACAGGAGCTGAAGGGCC 357
SEQID9    GGGCACTTCCTG-----CAAGATAA------------------------------------ 306
          **  **         *

SEQID5    TACACCAGGAGAATCATGGAACAGTCGACACACTTTCAGCTTAGTTTGAGAGATTGATTT 900
SEQID6    TACACCAGGAGAATCATGGAACAGTCGACACACTTTCAGCTTAGTTTGAGAGATTGATTT 832
SEQID7    TACACCAGGAGAATCATGGAACAGTCGACACACTTTCAGCTTAGTTTGAGAGATTGATTT 857
SEQID8    ACGGGCTTCCCCGGAACCCCTGGCAGGAAAGGAGAGCCTGGAGAAGCCGCTTATGTGTA 417
SEQID9    ------------------------------------------------------------

SEQID5    TATTGCTTAGTTTGAGAGTCCTGAGTATTATCCACACGTGTACTCACTTGTTCATTAAAC 960
SEQID6    TATTGCTTAGTTTGAGAGTCCTGAGTATTATCCACACGTGTACTCACTTGTTCATTAAAC 892
SEQID7    TATTGCTTAGTTTGAGAGTCCTGAGTATTATCCACACGTGTACTCACTTGTTCATTAAAC 917
SEQID8    TCGCTCAGCGTTCAGTGTGGGGCTGGAGACCCGCGTCACTGTTCCCAATGTACCCATTCG 477
SEQID9    ------------------------------------------------------------

SEQID5    GACTTTATAAAAAATAATTTGTGTTCCTAGTCCAGAAAAAAAGGCACTCCCTGGTCTCCA 1020
SEQID6    GACTTTATAAAAAATAATTTGTGTTCCTAGTCCAGAAAAAAAGGCACTCCCTGGTCTCCA 952
SEQID7    GACTTTATAAAAAATAATTTGTGTTCCTAGTCCAGAAAAAAAGGCACTCCCTGGTCTCCA 977
SEQID8    CTTTACTAAGATCTTCTACAACCAACAGAATCATTATGACGGCAGCACTGGCAAGTTCTA 537
SEQID9    ------------------------------------------------------------

SEQID5    CGACTCTTACATGGTAGCAATAACAGAATGAAAATCACATTTGGTATGGGGGCTTCACAA 1080
SEQID6    CGACTCTTACATGGTAGCAATAACAGAATGAAAATCACATTTGGTATGGGGGCTTCACAA 1012
SEQID7    CGACTCTTACATGGTAGCAATAACAGAATGAAAATCACATTTGGTATGGGGGCTTCACAA 1037
SEQID8    CTGCAACATTCCGGGACTCTACATTTACTGGCTTTCTTCTCTACCATGATACCAACTGAC 597
SEQID9    ------------------------------------------------------------

SEQID5    TATTCGCATGACTGTCTGGAAGTAGACCATGCTATTTTTCTGCTCACTGTACACAAATAT 1140
SEQID6    TATTCGCATGACTGTCTGGAAGTAGACCATGCTATTTTTCTGCTCACTGTACACAAATAT 1072
SEQID7    TATTCGCATGACTGTCTGGAAGTAGACCATGCTATTTTTCTGCTCACTGTACACAAATAT 1097
SEQID8    TGCAACTACCCATAGCCCATACACCAGGAGAATCATGGAACAGTCGACACACTTTCAGCT 657
SEQID9    ------------------------------------------------------------

SEQID5    TGTTCACATAAACCCTATAATGTAAATATGAAATACAGTGATTACTCTTCTCACAGGCTG 1200
SEQID6    TGTTCACATAAACCCTATAATGTAAATATGAAATACAGTGATTACTCTTCTCACAGGCTG 1132
SEQID7    TGTTCACATAAACCCTATAATGTAAATATGAAATACAGTGATTACTCTTCTCACAGGCTG 1157
SEQID8    TAGTTTGAGAGATTGATTTTATTGCTTAGTTTGAGAGTCCTGAGTATTATCCACACGTGT 717
SEQID9    ------------------------------------------------------------
```

```
SEQID5    ASTGTATGAATTCTAAAGACCCATAAGTATTAAAGTGGTAGGGATAAATTGGAAAAAAAA 1260
SEQID6    AGTGTATGAATTCTAAAGACCCATAAGTATTAAAGTGGTAGGGATAAATTGG-------- 1184
SEQID7    AGTGTATGAATTCTAAAGACCCATAAGTATTAAAGTGGTAGGGATAAATTGG-------- 1209
SEQID8    ACTCACTTGTTCATTAAACGACTTTATAAAAAATAATTTGTGTTCCTAGTCCAGAAAAAA 777
SEQID9    ------------------------------------------------------------


SEQID5    AAAAAAAAAAAGAAAAACTTTAGAGCACACTGGCGGCCGTTACTAG-------------- 1306
SEQID6    ------------------------------------------------------------
SEQID7    ------------------------------------------------------------
SEQID8    AGGCACTCCCTGGTCTCCACGACTCTTACATGGTAGCAATAACAGAATGAAAATCACATT 837
SEQID9    ------------------------------------------------------------


SEQID5    ------------------------------------------------------------
SEQID6    ------------------------------------------------------------
SEQID7    ------------------------------------------------------------
SEQID8    TGGTATGGGGGCTTCACAATATTCGCATGACTGTCTGGAAGTAGACCATGCTATTTTTCT 897
SEQID9    ------------------------------------------------------------


SEQID5    ------------------------------------------------------------
SEQID6    ------------------------------------------------------------
SEQID7    ------------------------------------------------------------
SEQID8    GCTCACTGTACACAAATATTGTTCACATAAACCCTATAATGTAAATATGAAATACAGTGA 957
SEQID9    ------------------------------------------------------------


SEQID5    ------------------------------------------------------------
SEQID6    ------------------------------------------------------------
SEQID7    ------------------------------------------------------------
SEQID8    TTACTCTTCTCACAGGCTGAGTGTATGAATTCTAAAGACCCATAAGTATTAAAGTGGTAG 1017
SEQID9    ------------------------------------------------------------


SEQID5    -----------
SEQID6    -----------
SEQID7    -----------
SEQID8    GGATAAATTGG 1028
SEQID9    -----------
```

Fig 8.

```
SEQID10   ACTCTGGATGGGTGCTGTTTAGACAAACGCCGTCTCCTATATAAGACCTGACAGCACAGG 60
SEQID11   ACTCTGGATGGGTGCTGTTTAGACAAACGCCGTCTCCTATATAAGACCTGACAGCACAGG 60
          ************************************************************

SEQID10   CACCACTCCGCCAGGACTGCAGGCCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCC 120
SEQID11   CACCACTCCGCCAGGACTGCAGGCCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCC 120
          ************************************************************

SEQID10   CCAGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCA 180
SEQID11   CCAGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCA 180
          ************************************************************

SEQID10   GGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGCAAAGGAGTCGAAGAAG 240
SEQID11   GGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG--GTGAGACCTCCCCACAAAG 238
          *******************************   *  * * **    * *  ***

SEQID10   CCACCCAGCCAAGCTGCAGCCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGGAAGATGGAGGT 300
SEQID11   CCCCCACATGTTGTTCCAGCCCTGCCCACTTAGCAA-CCAGCTCTGT----------GACCT 287
          ** *      * * ****** *    ***** * **** *         ** *

SEQID10   CAAGCAGAAGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTGATGTTGGA 360
SEQID11   GGAGCAGCAGCGCCATCTC-TGGGCTTCA-GTCTTCTCCCAGAGCACAAAGGACTCTGGG 345
          ***** ** * **       ** **  * ***   * * *  * *    **   ***

SEQID10   ATCAAGCTGTCAGGGGTTCAGTACCAGCAGCACAGCC--AGGCCCTGGGGAAGTTTCTTC 418
SEQID11   TCTGACCT--CACTGTTTCTGGAAGGACATGGGGGCTTAGAGTCCTAAACAGACTGTTTC 403
          * **  ** * *** * *  **      * *  ***  * ** *   * ***

SEQID10   AGGACATCCTCTGGGAAGAG-GCCAAAGAGGCCCCAGCCGACAAGTGATCGCCCACAAGC 477
SEQID11   CCCCTTCCAGCAGAGAAAGGAGTCGAAGAAGCC--ACCAGCCAAGCTGCAGCCC-CGAGC 460
          * * * **** * ** *** ***  *  * ***   **** *  *  ***

SEQID10   CTTACTCACCTCTCTCTAAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGC 537
SEQID11   TCTAGCAGGCTGGCTCC--GCCCGGAAGA-------TGGA---------GGTCAAGCAGA 502
           **     **  ***    *    ****    ***      * *  ****

SEQID10   AACTCCCACGACTGTTGTACAAGCTCAGGAGGCGAATAAATGTTCAAACTGTATGCTGAT 597
SEQID11   AGGGGCAGAGGATGAACTGGAAGTCCGGG---TCGGTACCTCTGCAG-TTTTATGCTTCT 558
          *     *   **    *  ***  * **       ** * * **  * ****** *

SEQID10   GTTCCAAATGGGAATTTATTTCAAAGAGGAAAAGTTAATATTTTACTTTAAAAAAATCAA 657
SEQID11   GTGGCAGCGAGGAGGGTGGGG----------------------------------------- 579
          ** **  *** *

SEQID10   AATAATAC 665
SEQID11   --------
```

Fig 9.

```
SEQID15     ------------------------------------------------------------
SEQID17     GGTGAAAAGGGAAAACCTGCCCAAATCCAGTTTTTGTTCAGTAACTTCCTTTGAGACAA  60
SEQID16     ------------------------------------------------------------
SEQID12     ------------------------------------------------------------
SEQID14     ------------------------------------------------------------
SEQID18     ------------------------------------------------------------
SEQID13     ------------------------------------------------------------


SEQID15     ------------------------------------------------------------
SEQID17     AGTCAGGAATCTGAGAGTAAGCACCTGCTAAGGGTGGGACAGGGGCTCTGTCTGGTATGC  120
SEQID16     ------------------------------------------------------------
SEQID12     ------------------------------------------------------------
SEQID14     ------------------------------------------------------------
SEQID18     ------------------------------------------------------------
SEQID13     ------------------------------------------------------------


SEQID15     ------------------------------------------------------------
SEQID17     CTCTCCCATGTTAAGAGCTAACAATAGTAATGGATAAGTCTCCAGGGCAACCAGGACCAC  180
SEQID16     ------------------------------------------------------------
SEQID12     ------------------------------------------------------------
SEQID14     ------------------------------------------------------------
SEQID18     ------------------------------------------------------------
SEQID13     ------------------------------------------------------------


SEQID15     ------------------------------------------------------------
SEQID17     TTCCAAGCATTCCTGTCTTGGGCTGCCTCGAGGGCTCCTCTGTCCTTTGGGGAGTACTGA  240
SEQID16     ------------------------------------------------------------
SEQID12     ------------------------------------------------------------
SEQID14     ------------------------------------------------------------
SEQID18     ------------------------------------------------------------
SEQID13     ------------------------------------------------------------


SEQID15     ------------------------------------------------------------
SEQID17     TTGATGCCTGATGCCCAGAACTGGCCCACTCTGGCTTCTCTTTGGAGCTGTCTCTGCAGG  300
SEQID16     ------------------------------------------------------------
SEQID12     ------------------------------------------------------------
SEQID14     ------------------------------------------------------------
SEQID18     ------------------------------------------------------------
SEQID13     ------------------------------------------------------------


SEQID15     ---------------------------------------------------------GCA  3
SEQID17     CGCCTTCTGGCTGCCAGCTCGGTCCTAGCATRAGGGACTTCTTCCTTGGCCTGGGTTTCA  360
SEQID16     ---------------------------------------------------------GCA  3
SEQID12     ---------------------------------------------------------GCA  3
SEQID14     ---------------------------------------------------------GCA  3
SEQID18     ---------------------------------------------------------GCA  3
SEQID13     ---------------------------------------------------------GCA  3
                                                                     **

SEQID15     CTGCCTGAGACTACTC--CAGCCTCCCCGTCCCTGATGTCACAATTCAGAGGCTGCTGC  61
SEQID17     CCTTCTTGTATCAGGTGGCAGACCAGCTGGTTTCAG---TCCCAAATCAG-GTCTTCTGA  416
SEQID16     CTGCCTGAGACTACTC--CAGCCTCCCCGTCCCTGATGTCACAATTCAGAGGCTGCTGC  61
SEQID12     CTGCCTGAGACTACTC--CAGCCTCCCCGTCCCTGATGTCACAATTCAGAGGCTGCTGC  61
SEQID14     CTGCCTGAGACTACTC--CAGCCTCCCCGTCCCTGATGTCACAATTCAGAGGCTGCTGC  61
SEQID18     CTGCCTGAGACTACTC--CAGCCTCCCCGTCCCTGATGTCACAATTCAGAGGCTGCTGC  61
SEQID13     CTGCCTGAGACTACTC--CAGCCTCCCCGTCCCTGATGTCACAATTCAGAGGCTGCTGC  61
            *  **   *  *     *** *   *  ** *  *  ** *** **** * ** ***

SEQID15     CTGCTTAGGAGGTTGTAGAAAGCTCTG--TAGGTTCTCTCTGTGTGTCCTACAGGAGTCT  119
SEQID17     CTCCTCCCAGAAACCAACCAACTTCTGAGCAGGAAATC-CTGCCCCTCCCCAAAGAGTGG  475
SEQID16     CTGCTTAGGAGGTTGTAGAAAGCTCTG--TAGGTTCTCTCTGTGTGTCCTACAGGAGTCT  119
SEQID12     CTGCTTAGGAGGTTGTAGAAAGCTCTG--TAGGTTCTCTCTGTGTGTCCTACAGGAGTCT  119
```

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SEQID14    CTGCTTAGGAGGTTGTAGAAAGCTCTG--TAGGTTCTCTCTGTGTGTCCTACAGGAGTCT 119
SEQID18    CTGCTTAGGAGGTTGTAGAAAGCTCTG--TAGGTTCTCTCTGTGTGTCCTACAGGAGTCT 119
SEQID13    CTGCTTAGGAGGTTGTAGAAAGCTCTG--TAGGTTCTCTCTGTGTGTCCTACAGGAGTCT 119
           ** **        *  **  ****  ***   ** ***    ***  * ****

SEQID15    TCAG--GCCAGCTCCCTGTCGGATGGCTTTTATGAAAAAATATCTCCTCCCCATTCTGGG 177
SEQID17    GAAACCGCAAAGGAAGAGAGATGAAACAGAAGGAAAGGCAGAGGAGGGAGGGAGAGAGA 535
SEQID16    TCAG--GCCAGCTCCCTGTCGGATGGCTTTTATGAAAAAATATCTCCTCCCCATTCTGGG 177
SEQID12    TCAG--GCCAGCTCCCTGTCGGATGGCTTTTATGAAAAAATATCTCCTCCCCATTCTGGG 177
SEQID14    TCAG--GCCAGCTCCCTGTCGGATGGCTTTTATGAAAAAATATCTCCTCCCCATTCTGGG 177
SEQID18    TCAG--GCCAGCTCCCTGTCGGATGGCTTTTATGAAAAAATATCTCCTCCCCATTCTGGG 177
SEQID13    TCAG--GCCAGCTCCCTGTCGGATGGCTTTTATGAAAAAATATCTCCTCCCCATTCTGGG 177
            *  ** *      *  ****   ****   * *** *   ***   *

SEQID15    GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTCAGACC---------- 225
SEQID17    GAGAAGAGAAGAAAAAGAAAAAGAACATCAATAAAAAGAAGTCAGATTTGTTCGAAATC 595
SEQID16    GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTCAGACC---------- 225
SEQID12    GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTCAGACC---------- 225
SEQID14    GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTCAGACC---------- 225
SEQID18    GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTCAGACC---------- 225
SEQID13    GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTCAGACC---------- 225
            *      *   *    *  *  *** *  * *** ***** 

SEQID15    ---AGAGATGCTCCAAGGAAAGAAAGTGATTGTCACAGGGGCCAGCAAAGGGATCGGAAG 282
SEQID17    TTGAGAGATGCTCCAAGGAAAGAAAGTGATTGTCACAGGGGCCAGCAAAGGGATCGGAAG 655
SEQID16    ---AGAGATGCTCCAAGGAAAGAAAGTGATTGTCACAGGGGCCAGCAAAGGGATCGGAAG 282
SEQID12    ---AGAGATGCTCCAAGGAAAGAAAGTGATTGTCACAGGGGCCAGCAAAGGGATCGGAAG 282
SEQID14    ---AGAGATGCTCCAAGGAAAGAAAGTGATTGTCACAGGGGCCAGCAAAGGGATCGGAAG 282
SEQID18    ---AGAGATGCTCCAAGGAAAGAAAGTGATTGTCACAGGGGCCAGCAAAGGGATCGGAAG 282
SEQID13    ---AGAGATGCTCCAAGGAAAGAAAGTGATTGTCACAGGGGCCAGCAAAGGGATCGGAAG 282
              **************************************************

SEQID15    AGAGATGGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGAGGTCAAA 342
SEQID17    AGAGATGGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGAGGTCAAA 715
SEQID16    AGAGATGGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGAG------ 336
SEQID12    AGAGATGGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGAGGTCAAA 342
SEQID14    AGAGATGGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGAGGTCAAA 342
SEQID18    AGAGATGGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGAGGTCAAA 342
SEQID13    AGAGATGGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGAG------ 336
           *****************************************************

SEQID15    AGAAACTCTACAGAAGGTGGTATCCCACTGCCTGGAGCTTGGAGCAGCCTCAGCACACTA 402
SEQID17    AGAAACTCTACAGAAGGTGGTATCCCACTGCCTGGAGCTTGGAGCAGCCTCAGCACACTA 775
SEQID16    ------------------------------------------CTCAGCACACTA 348
SEQID12    AGAAACTCTACAGAAGGTGGTATCCCACTGCCTGGAGCTTGGAGCAGCCTCAGCACACTA 402
SEQID14    AGAAACTCTACAGAAGGTGGTATCCCACTGCCTGGAGCTTGGAGCAGCCTCAGCACACTA 402
SEQID18    AGAAACTCTACAGAAGGTGGTATCCCACTGCCTGGAGCTTGGAGCAGCCTCAGCACACTA 402
SEQID13    ------------------------------------------CTCAGCACACTA 348
                                                       ************

SEQID15    CATTGCTGGCACCATGGAAGACATGACCTTCGCAGAGCAATTTGTTGCCCAAGCAGGAAA 462
SEQID17    CATTGCTGGCACCATGGAAGACATGACCTTCGCAGAGCAATTTGTTGCCCAAGCAGGAAA 835
SEQID16    CATTGCTGGCACCATGGAAGACATGACCTTCGCAGAGCAATTTGTTGCCCAAGCAGGAAA 468
SEQID12    CATTGCTGGCACCATGGAAGACATGACCTTCGCAGAGCAATTTGTTGCCCAAGCAGGAAA 462
SEQID14    CATTGCTGGCACCATGGAAGACATGACCTTCGCAGAGCAATTTGTTGCCCAAGCAGGAAA 462
SEQID18    CATTGCTGGCACCATGGAAGACATGACCTTCGCAGAGCAATTTGTTGCCCAAGCAGGAAA 462
SEQID13    CATTGCTGGCACCATGGAAGACATGACCTTCGCAGAGCAATTTGTTGCCCAAGCAGGAAA 408
           ************************************************************

SEQID15    GCTCATGGGAGGACTAGACATGCTCATTCTCAACCACATCACCAACACTTCTTTGAATCT 522
SEQID17    GCTCATGGGAGGACTAGACATGCTCATTCTCAACCACATCACCAACACTTCTTTGAATCT 895
SEQID16    GCTCATGGGAGGACTAGACATGCTCATTCTCAACCACATCACCAACACTTCTTTGAATCT 468
SEQID12    GCTCATGGGAGGACTAGACATGCTCATTCTCAACCACATCACCAACACTTCTTTGAATCT 522
SEQID14    GCTCATGGGAGGACTAGACATGCTCATTCTCAACCACATCACCAACACTTCTTTGAATCT 522
SEQID18    GCTCATGGGAGGACTAGACATGCTCATTCTCAACCACATCACCAACACTTCTTTGAATCT 522
SEQID13    GCTCATGGGAGGACTAGACATGCTCATTCTCAACCACATCACCAACACTTCTTTGAATCT 468
           ************************************************************

SEQID15    TTTTCATGATGATATTCACCATGTGCGC-------------------------------- 550
SEQID17    TTTTCATGATGATATTCACCATGTGCGCAAAAGCATGGAAGTCAACTTCCTCAGTTACGT 955
SEQID16    TTTTCATGATGATATTCACCATGTGCGCAAAAGCATGGAAGTCAACTTCCTCAGTTACGT 528
```

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SEQID12    TTTTCATGATGATATTCACCATGTGCGCAAAAGCATGGAAGTCAACTTCCTCAGTTACGT 582
SEQID14    TTTTCATGATGATATTCACCATGTGCGCAAAAGCATGGAAGTCAACTTCCTCAGTTACGT 582
SEQID18    TTTTCATGATGATATTCACCATGTGCGCAAAAGCATGGAAGTCAACTTCCTCAGTTACGT 582
SEQID13    TTTTCATGATGATATTCACCATGTGCGCAAAAGCATGGAAGTCAACTTCCTCAGTTACGT 528
           ***************************

SEQID15    ---------------------CCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT 588
SEQID17    GGTCCTGACTGTAGCTGCCTTGCCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT 1015
SEQID16    GGTCCTGACTGTAGCTGCCTTGCCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT 588
SEQID12    GGTCCTGACTGTAGCTGCCTTGCCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT 642
SEQID14    GGTCCTGACTGTAGCTGCCTTGCCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT 642
SEQID18    GGTCCTGACTGTAGCTGCCTTGCCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT 642
SEQID13    GGTCCTGACTGTAGCTGCCCATGCTGAAGCAGAGCAATGGAAGCAT------GT 581
                                       ****************************   **

SEQID15    CTCCTCTCTGGCTGGGAAAGTGGCTTATCCAATGGTTGCTGCC-TATTCTGCAAGCAAGT 647
SEQID17    CTCCTCTCTGGCTGGGAAAGTGGCTTATCCAATGGTTGCTGCC-TATTCTGCAAGCAAGT 1074
SEQID16    CTCCTCTCTGGCTGGGAAAGTGGCTTATCCAATGGTTGCTGCC-TATTCTGCAAGCAAGT 647
SEQID12    CTCCTCTCTGGCTGGGAAAGTGGCTTATCCAATGGTTGCTGCC-TATTCTGCAAGCAAGT 701
SEQID14    CTCCTCTCTGGCTGGGAAAGTGGCTTATCCAATGGTTGCTGCC-TATTCTGCAAGCAAGT 701
SEQID18    CTCCTCTCTGGCTG---------------------------------------------- 656
SEQID13    GCGCTCTTCTGCTGGAA-------------------TGCTATCATGTTGTGCATCTGAGC 622
             ****   ****

SEQID15    TTGCTTTGGATGGGTTCTTCTCCTCCATCAGAAAGGAATATTCAGTGTCCAGGGTCAATG 707
SEQID17    TTGCTTTGGATGGGTTCTTCTCCTCCATCAGAAAGGAATATTCAGTGTCCAGGGTCAATG 1134
SEQID16    TTGCTTTGGATGGGTTCTTCTCCTCCATCAGAAAGGAATATTCAGTGTCCAGGGTCAATG 707
SEQID12    TTGCTTTGGATGGGTTCTTCTCCTCCATCAGAAAGGAATATTCAGTGTCCAGGGTCAATG 761
SEQID14    TTGCTTTGGATGGGTTCTTCTCCTCCATCAGAAAGGAATATTCAGTGTCCAGGGTCAATG 761
SEQID18    ------------------------------------------------------------
SEQID13    A-GTNGTTGATGG-----TCTCTCTCAT----AGAAGATATCAGG----CAGGCATGATA 668

SEQID15    TATCAATCACTCTCTGTGTTCTTGGCCTCATAGACACAGAAACAGCCATG-AAGGCAGTT 766
SEQID17    TATCAATCACTCTCTGTGTTCTTGGCCTCATAGACACAGAAACAGCCATG-AAGGCAGTT 1193
SEQID16    TATCAATCACTCTCTGTGTTCTTGGCCTCATAGACACAGAAACAGCCATG-AAGGCAGTT 766
SEQID12    TATCAATCACTCTCTGTGTTCTTGGCCTCATAGACACAGAAACAGCCATG-AAGGCAGTT 820
SEQID14    TATCAATCACTCTCTGTGTTCTTGGCCTCATAGACACAGAAACAGCCATG-AAGGCAGTT 820
SEQID18    ---------------------------------AAACAGCCATG-AAGGCAGTT 676
SEQID13    TACT------------------TTGGTCTGCTATACCAGACGCTAGGCGTCTGATGCA--- 708
                                             ** * *    * ***

SEQID15    TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAAA 826
SEQID17    TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAAA 1253
SEQID16    TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAAA 826
SEQID12    TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAAA 880
SEQID14    TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAAA 880
SEQID18    TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAAA 736
SEQID13    ------------------------------------------------------------

SEQID15    GGGGGAGCTCTGCGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTTCTG 886
SEQID17    GGGGGAGCTCTGCGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTTCTG 1313
SEQID16    GGGGGAGCTCTGCGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTTCTG 886
SEQID12    GGGGGAGCTCTGCGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTTCTG 940
SEQID14    GGGGGAGCTCTGCGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTTCTG 940
SEQID18    GGGGGAGCTCTGCGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTTCTG 796
SEQID13    ------------------------------------------------------------

SEQID15    ATCAGAAATCCATGCAGGAAGATCCTGGAATTTCTCTACTCAACGAGCTATAATATGGAC 946
SEQID17    ATCAGAAATCCATGCAGGAAGATCCTGGAATTTCTCTACTCAACGAGCTATAATATGGAC 1373
SEQID16    ATCAGAAATCCATGCAGGAAGATCCTGGAATTTCTCTACTCAACGAGCTATAATATGGAC 946
SEQID12    ATCAGAAATCCATGCAGGAAGATCCTGGAATTTCTCTACTCAACGAGCTATAATATGGAC 1000
SEQID14    ATCAGAAATCCATGCAGGAAGATCCTGGAATTTCTCTACTCAACGAGCTATAATATGGA- 999
SEQID18    ATCAGAAATCCATGCAGGAAGATCCTGGAATTTCTCTACTCAACGAGCTATAATATGGAC 856
SEQID13    ------------------------------------------------------------

SEQID15    AGATTCATAAACAAGTAGGAACTCCCTGAGGGCTGGGCATGCTGAGGGATTTTGGGACTG 1006
SEQID17    AGATTCATAAACAAGTAGGAACTCCCTGAGGGCTGGGCATGCTGAGGGATTTTGGGACTG 1433
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·SEQID16   AGATTCATAAACAAGTAGGAACTCCCTGAGGGCTGGGCATGCTGAGGGATTTTGGGACTG 1006
 SEQID12   AGATTCATAAACAAGTAGGAACTCCCTGAGGGCTGGGCATGCTGAGGGATTTTGGGACTG 1060
 SEQID14   ------------------------------------------------------GGGACTG 1006
 SEQID18   AGATTCATAAACAAGTAGGAACTCCCTGAGGGCTGGGCATGCTGAGGGATTTTGGGACTG  916
 SEQID13   ------------------------------------------------------------


 SEQID15   TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTTCCCAGAGTGTCCCCAG 1066
 SEQID17   TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTTCCCAGAGTGTCCCCAG 1493
 SEQID16   TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTTCCCAGAGTGTCCCCAG 1066
 SEQID12   TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTTCCCAGAGTGTCCCCAG 1120
 SEQID14   TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTTCCCAGAGTGTCCCCAG 1066
 SEQID18   TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTTCCCAGAGTGTCCCCAG  976
 SEQID13   ------------------------------------------------------------


 SEQID15   AGACATGCAAGTCATGGGTCACACCTGACAAATGGAAGGAGTTCCTCTAACATTTGCAAA 1126
 SEQID17   AGACATGCAAGTCATGGGTCACACCTGACAAATGGAAGGAGTTCCTCTAACATTTGCAAA 1553
 SEQID16   AGACATGCAAGTCATGGGTCACACCTGACAAATGGAAGGAGTTCCTCTAACATTTGCAAA 1126
 SEQID12   AGACATGCAAGTCATGGGTCACACCTGACAAATGGAAGGAGTTCCTCTAACATTTGCAAA 1180
 SEQID14   AGACATGCAAGTCATGGGTCACACCTGACAAATGGAAGGAGTTCCTCTAACATTTGCAAA 1126
 SEQID18   AGACATGCAAGTCATGGGTCACACCTGACAAATGGAAGGAGTTCCTCTAACATTTGCAAA 1036
 SEQID13   ------------------------------------------------------------


 SEQID15   ATGGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAAAATTGTT 1186
 SEQID17   ATGGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAAAATTGTT 1613
 SEQID16   ATGGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAAAATTGTT 1186
 SEQID12   ATGGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAAAATTGTT 1240
 SEQID14   ATGGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAAAATTGTT 1186
 SEQID18   ATGGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAAAATTGTT 1096
 SEQID13   ------------------------------------------------------------


 SEQID15   AGTAAACATAGGTATAATTACCAGATAGTTATATTAAATTTATATCTTATATATAATAAT 1246
 SEQID17   AGTAAACATAGGTATAATTACCAGATAGTTATATTAAATTTATATCTTATATATAATAAT 1673
 SEQID16   AGTAAACATAGGTATAATTACCAGATAGTTATATTAAATTTATATCTTATATATAATAAT 1246
 SEQID12   AGTAAACATAGGTATAATTACCAGATAGTTATATTAAATTTATATCTTATATATAATAAT 1300
 SEQID14   AGTAAACATAGGTATAATTACCAGATAGTTATATTAAATTTATATCTTATATATAATAAT 1246
 SEQID18   AGTAAACATAGGTATAATTACCAGATAGTTATATTAAATTTATATCTTATATATAATAAT 1156
 SEQID13   ------------------------------------------------------------


 SEQID15   ATGTGATGATTAATACAATATTAATTATAATAAAGGTCACATAAACTTTATAAATTCATA 1306
 SEQID17   ATGTGATGATTAATACAATATTAATTATAATAAAGGTCACATAAACTTTATAAATTCATA 1733
 SEQID16   ATGTGATGATTAATACAATATTAATTATAATAAAGGTCACATAAACTTTATAAATTCATA 1306
 SEQID12   ATGTGATGATTAATACAATATTAATTATAATAAAGGTCACATAAACTTTATAAATTCATA 1360
 SEQID14   ATGTGATGATTAATACAATATTAATTATAATAAAGGTCACATAAACTTTATAAATTCATA 1306
 SEQID18   ATGTGATGATTAATACAATATTAATTATAATAAAGGTCACATAAACTTTATAAATTCATA 1216
 SEQID13   ------------------------------------------------------------


 SEQID15   ACTGGTAGCTATAACTTGAGCTTATTCAGGATGGTTCTTTAAAACCATAAACTGTACAA 1366
 SEQID17   ACTGGTAGCTATAACTTGAGCTTATTCAGGATGGTTCTTTAAAACCATAAACTGTACAA 1793
 SEQID16   ACTGGTAGCTATAACTTGAGCTTATTCAGGATGGTTCTTTAAAACCATAAACTGTACAA 1366
 SEQID12   ACTGGTAGCTATAACTTGAGCTTATTCAGGATGGTTCTTTAAAACCATAAACTGTACAA 1420
 SEQID14   ACTGGTAGCTATAACTTGAGCTTATTCAGGATGGTTCTTTAAAACCATAAACTGTACAA 1366
 SEQID18   ACTGGTAGCTATAACTTGAGCTTATTCAGGATGGTTCTTTAAAACCATAAACTGTACAA 1276
 SEQID13   ------------------------------------------------------------


 SEQID15   ATGAAATTTTTCAATATTTGTTTCTTAT 1394
 SEQID17   ATGAAATTTTTCAATATTTGTTTCTTAT 1821
 SEQID16   ATGAAATTTTTCAATATTTGTTTCTTAT 1394
 SEQID12   ATGAAATTTTTCAATATTTGTTTCTTAT 1448
 SEQID14   ATGAAATTTTTCAATATTTGTTTCTTAT 1394
 SEQID18   ATGAAATTTTTCAATATTTGTTTCTTAT 1304
 SEQID13   ---------------------------
```

Fig 10.

```
SEQID19   ACTGTTGGCCTCTGGAWTCAGAGGCTGCTGCCTGCCTGGGAGGTTGTAGAAAGCTCTGCA 60
SEQID20   ACTGTTGGCCTCTGGAWTCAGAGGCTGCTGCCTGCCTGGGAGGTTGTAGAAAGCTCTGCA 60
SEQID21   ACTGTTGGCCTCTGGAWTCAGAGGCTGCTGCCTGCCTGGGAGGTTGTAGAAAGCTCTGCA 60
          ************************************************************

SEQID19   GGTTTTCTTCGTGTGTCCTACAGGGCGCCCTGAGCCAGGTCCCTGTTTGATGGCAGTTAT 120
SEQID20   GGTTTTCTTCGTGTGTCCTACAGGGCGCCCTGAGCCAGGTCCCTGTTTGATGGCAGTTAT 120
SEQID21   GGTTTTCTTCGTGTGTCCTACAGGGCGCCCTGAGCCAGGTCCCTGTTTGATGGCAGTTAT 120
          ************************************************************

SEQID19   GAAAAATTACCTCCTCCCGATCCTGGTGCTCTTCCTGGCCTACTACTACTATTCTACAAA 180
SEQID20   GAAAAATTACCTCCTCCCGATCCTGGTGCTCTTCCTGGCCTACTACTACTATTCTACAAA 180
SEQID21   GAAAAATTACCTCCTCCCGATCCTGGTGCTCTTCCTGGCCTACTACTACTATTCTACAAA 180
          ************************************************************

SEQID19   TGAAGAGTTCAGACCAGAAATGCTCCAGGGAAAGAAAGTGATTGTCACTGGGGCCAGCAA 240
SEQID20   TGAAGAGTTCAGAC----------------------------------------------- 194
SEQID21   TGAAGAGTTCAGACCAGAAATGCTCCAGGGAAAGAAAGTGATTGTCACTGGGGCCAGCAA 240
          **************

SEQID19   AGGGATTGGAAGAGAAATGGCATATCATCTGTCAAAAATGGGAGCCCATGTGGTATTGAC 300
SEQID20   ------------------------------------------------------------
SEQID21   AGGGATTGGAAGAGAAATGGCATATCATCTGTCAAAAATGGGAGCCCATGTGGTATTGAC 300


SEQID19   TGCCAGGTCGGAGGAAGGTCTCCAGAAGGTAGTGTCTCGCTGCCTTGAACTCGGAGCAGC 360
SEQID20   --------------------TCCAGAAGGTAGTGTCTCGCTGCCTTGAACTCGGAGCAGC 234
SEQID21   TGCCAGGTCGGAGGAAGGTCTCCAGAAGGTAGTGTCTCGCTGCCTTGAACTCGGAGCAGC 360
                              ***************************************

SEQID19   CTCTGCTCACTACATTGCTGGCACTATGGAAGACATGACATTTGCGGAGCAATTTATTGT 420
SEQID20   CTCTGCTCACTACATTGCTGGCACTATGGAAGACATGACATTTGCGGAGCAATTTATTGT 294
SEQID21   CTCTGCTCACTACATTGCTGGCACTATGGAAGACATGACATTTGCGGAGCAATTTATTGT 420
          ************************************************************

SEQID19   CAAGGCGGGAAAGCTCATGGGCGGACTGGACATGCTTATTCTAAACCACATCACTCAGAC 480
SEQID20   CAAGGCGGGAAAGCTCATGGGCGGACTGGACATGCTTATTCTAAACCACATCACTCAGAC 354
SEQID21   CAAGGCGGGAAAGCTCATGGGCGGACTGGACATGCTTATTCTAAACCACATCACTCAGAC 480
          ************************************************************

SEQID19   CTCGCTGTCTCTCTTCCATGACGACATCCACTCTGTGCGAAGAGTCATGGAGGTCAACTT 540
SEQID20   CTCGCTGTCTCTCTTCCATGACGACATCCACTCTGTGCGAAGAGTCATGGAGGTCAACTT 414
SEQID21   CTCGCTGTCTCTCTTCCATGACGACATCCACTCTGTGCGAAGAGTCATGGAGGTCAACTT 540
          ************************************************************

SEQID19   CCTCAGCTACGTGGTCATGAGCACAGCCGCCTTGCCCATGCTGAAGCAGAGCAATGGCAG 600
SEQID20   CCTCAGCTACGTGGTCATGAGCACAGCCGCCTTGCCCATGCTGAAGCAGAGCAATGGCAG 474
SEQID21   CCTCAGCTACGTGGTCATGAGCACAGCCGCCTTGCCCATGCTGAAGCAGAGCAATGGCAG 600
          ************************************************************

SEQID19   CATTGCCGTCATCTCCTCCTTGGCTGGGAAAATGACCCAGCCTATGATTGCTCCCTACTC 660
SEQID20   CATTGCCGTCATCTCCTCCTTGGCTGGGAAAATGACCCAGCCTATGATTGCTCCCTACTC 534
SEQID21   CATTGCCGTCATCTCCTCCTTGGCTGGGGGAA-GAACAGTTCCACAACAGAGA---AGTC 656
          ****************************     **  ***    * * *   *   * **

SEQID19   TGCAAGCAAGTTTGCTCTGGATGGGTTCTTTTCCACCATTAGAACAGAACTCTACATAAC 720
SEQID20   TGCAAGCAAGTTTGCTCTGGATGGGTTCTTTTCCACCATTAGAACAGAACTCTACATAAC 594
SEQID21   -----GCAGTGTTACTCCTGAC--------TCCCGC-----GGCCCGTGATTAATATCAC 698
              ***   ** ***  **         * * *     *   * * ***  * *

SEQID19   CAAGGTCAACGTGTCCATCACTCTCTGTGTCCTTGGCCTCATAGACACAGAAACAGCTAT 780
SEQID20   CAAGGTCAACGTGTCCATCACTCTCTGTGTCCTTGGCCTCATAGACACAGAAACAGCTAT 654
SEQID21   CAGCCACAGAATGGAC-TGGAACCCTGTATC---GATCTGGTGGGATTGGATATAACGAA 754
          **    **   ** *     * ****  **   *  ** * *     ** * * **

SEQID19   GAAGGAA--ATCTCTGGGATAATTAACGCCCAAGCTTCTCCCAAGGAGGAGTGCGCCCTG 838
SEQID20   GAAGGAA--ATCTCTGGGATAATTAACGCCCAAGCTTCTCCCAAGGAGGAGTGCGCCCTG 712
SEQID21   CATAGAATTACTCCTGAGACTACCAGAACTGAA---TAGTTCAAATCAAATCATGCC--- 808
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                       *  ***    *   *** **   *   *    *  **    *    ***      *    ***
SEQID19    GAGATCATCAAAGGCACAGCTCTACGCAAAAGCGAGGTGTACTATGACAAATCGCCTTTG 898
SEQID20    GAGATCATCAAAGGCACAGCTCTACGCAAAAGCGAGGTGTACTATGACAAATCGCCTTTG 772
SEQID21    -AGAATATC--AGACAAATCCAAATGGCAAAAC-AGTTGCA------------------- 845
           ***   ***   ** ** *  *   * *  *** *  ** ** *

SEQID19    ACTCCAATCCTGCTTGGGAACCCAGGAAGGAAGATCATGGAATTTTTTTCATTACGATAT 958
SEQID20    ACTCCAATCCTGCTTGGGAACCCAGGAAGGAAGATCATGGAATTTTTTTCATTACGATAT 832
SEQID21    -----------------------------------------------------------

SEQID19    TATAATAAGGACATGTTTGTAAGTAACTAGGAACTCCTGAGCCCTGGTGAGTGGTCTTAG 1018
SEQID20    TATAATAAGGACATGTTTGTAAGTAACTAGGAACTCCTGAGCCCTGGTGAGTGGTCTTAG 892
SEQID21    -----------------------------------------------------------

SEQID19    AACAGTCCTGCCTGATACTTCTGTAAGCCCTACCCACAAAAGTATCTTTCCAGAGATACA 1078
SEQID16    AACAGTCCTGCCTGATACTTCTGTAAGCCCTACCCACAAAAGTATCTTTCCAGAGATACA 952
SEQID21    -----------------------------------------------------------

SEQID19    CAAATTTTGGGGTACACCTCATCATGAGAAATTCTTGCAACACTTGCACAGTGAAAATGT 1138
SEQID20    CAAATTTTGGGGTACACCTCATCATGAGAAATTCTTGCAACACTTGCACAGTGAAAATGT 1012
SEQID21    -----------------------------------------------------------

SEQID19    AATTGTAATAAATGTCACAAACCACTTTGGGGCCTGCAGTTGTGAACTTGATTGTAACTA 1198
SEQID20    AATTGTAATAAATGTCACAAACCACTTTGGGGCCTGCAGTTGTGAACTTGATTGTAACTA 1072
SEQID21    -----------------------------------------------------------

SEQID19    TGGATATAAACACATAGTGGTTGTATCGGCTTTACCTCACACTGAATGAAACAATGATAA 1258
SEQID20    TGGATATAAACACATAGTGGTTGTATCGGCTTTACCTCACACTGAATGAAACAATGATAA 1132
SEQID21    -----------------------------------------------------------

SEQID19    CTAATGTAACATTAAATATAATAAAGGTAATATCAACTTTGTAAATGCA 1307
SEQID20    CTAATGTAACATTAAATATAATAAAGGTAATATCAACTTTGTAAATGCA 1181
SEQID21    ------------------------------------------------
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